SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: HighTech Receptro AB
        (B) STREET: c/o Active, Skeppsbron 2
        (C) CITY: MALMO
        (E) COUNTRY: SWEDEN
        (F) POSTAL CODE (ZIP): 211 20
        (G) TELEPHONE: 040/35 07 00
        (H) TELEFAX: 040/ 23 74 05
        (I) TELEX: 32637 Active S

    (ii) TITLE OF INVENTION: Hybridprotein

    (iii) NUMBER OF SEQUENCES: 1

    (iv) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(EPO)

    (v) CURRENT APPLICATION DATA:
        APPLICATION NUMBER: SE PCT/SE93/00375
    (vi) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: SE 9201331-7
        (B) FILING DATE: 28-APR-1992

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 305 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: unknown
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: protein

    (iii) HYPOTHETICAL: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
1               5                   10                  15

Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
            20                  25                  30

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
            35                  40                  45
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Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
    50   55   60

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
65   70   75   80

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
            85   90   95

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
            100   105   110

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
        115   120   125

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
    130   135   140

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
145   150   155   160

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
            165   170   175

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
        180   185   190

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
        195   200   205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
210   215   220

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
225   230   235   240

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
            245   250   255

Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
        260   265   270

Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
    275   280   285

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
290   295   300

Glu
305

(2) INFORMATION FOR SEQ ID NO: 2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 921 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA        50

AGAAGAAGTA ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC       100

AAACTGCAGA ATTCAAAGGA ACATTTGAAA AAGCAACATC AGAAGCTTAT       150

GCGTATGCAG ATACTTTGAA GAAAGACAAT GGAGAATATA CTGTAGATGT       200

TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA AAAGAAAAAA       250

CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT       300

GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC       350

AACAGCAGAA GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG       400

AATATACAGT AGACGTTGCA GATAAAGGTT ATACTTTAAA TATTAAATTT       450

GCTGGAAAAG AAAAAACACC AGAAGAACCA AAGAAGAAG TTACTATTAA        500

AGCAAACTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA GAATTCAAAG       550

GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA       600

GCAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC        650

TTTAAATATT AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG       700

AAGAAGTTAC TATTAAAGCA AACTTAATCT ATGCAGATGG AAAAACTCAA       750

ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA GCAACAGCAG AAGCATACAG       800

ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA GCAGACTTAG       850

AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC       900

GAAAAACCAG AAGAATAATA A                                      921
```

(2) INFORMATION FOR SEQ ID NO: 3:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 434 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: unknown
          (D) TOPOLOGY: unknown

     (ii) MOLECULE TYPE: protein

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    (iii) HYPOTHETICAL: NO

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
1               5               10              15

Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
            20              25              30

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
        35              40              45

Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
    50              55              60

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
65              70              75              80

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
            85              90              95

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
            100             105             110

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
        115             120             125

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
    130             135             140

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
145             150             155             160

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
            165             170             175

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
        180             185             190

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
    195             200             205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
    210             215             220

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
225             230             235             240

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
            245             250             255

Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
            260             265             270
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Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
        275   280   285

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
        290   295   300

Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
305   310   315   320

Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
                325   330   335

Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
            340   345   350

Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
        355   360   365

Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
        370   375   380

Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
385   390   395   400

Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
                405   410   415

Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
            420   425   430

Glu Met

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1308 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Escherichis coli L392/pHDLG, DSM 7055

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA   50

AGAAGAAGTA ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC   100

AAACTGCAGA ATTCAAAGGA ACATTTGAAA AAGCAACATC AGAAGCTTAT   150

GCGTATGCAG ATACTTTGAA GAAAGACAAT GGAGAATATA CTGTAGATGT   200

```
TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA AAAGAAAAAA        250

CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT        300

GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC        350

AACAGCAGAA GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG        400

AATATACAGT AGACGTTGCA GATAAAGGTT ATACTTTAAA TATTAAATTT        450

GCTGGAAAAG AAAAAACACC AGAAGAACCA AAAGAAGAAG TTACTATTAA        500

AGCAAACTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA GAATTCAAAG        550

GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA        600

GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC        650

TTTAAATATT AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG        700

AAGAAGTTAC TATTAAAGCA AACTTAATCT ATGCAGATGG AAAAACTCAA        750

ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA GCAACAGCAG AAGCATACAG        800

ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA GCAGACTTAG        850

AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC        900

GAAAAACCAG AAGAACCCAT GGACACTTAC AAATTAATCC TTAATGGTAA        950

AACATTGAAA GGCGAAACAA CTACTGAAGC TGTTGATGCT GCTACTGCAG        1000

AAAAAGTCTT CAAACAATAC GCTAACGACA ACGGTGTTGA CGGTGAATGG        1050

ACTTACGACG ATGCGACTAA GACCTTTACA GTTACTGAAA AACCAGAAGT        1100

GATCGATGCG TCTGAATTAA CACCAGCCGT GACAACTTAC AAACTTGTTA        1150

TTAATGGTAA AACATTGAAA GGCGAAACAA CTACTAAAGC AGTAGACGCA        1200

GAAACTGCAG AAAAAGCCTT CAAACAATAC GCTAACGACA ACGGTGTTGA        1250

TGGTGTTTGG ACTTATGATG ATGCGACTAA GACCTTTACG GTAACTGAAA        1300

TGTAATAA                                                     1308
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